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UNITED STATES DISTRICT COURT
SOUTHERN DISTRICT OF CALIFORNIA

ILLUMINA, INC. and ILLUMINA CAMBRIDGE LTD.,

Plaintiffs,

v.

COMPLETE GENOMICS, INC.,

Defendant.

Case No. 3:12-cv-01465-BEN-BGS

JOINT CLAIM CONSTRUCTION CHART

[Patent L.R. 4-2(a)]

Hon. Roger T. Benitez
Date: July 11, 2013
Time: 9:00 A.M.
Room: 4B

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JOINT CLAIM CONSTRUCTION CHART

Claim 1	Illumina's Proposed Constructions and Supporting Citations	CGI's Proposed Constructions and Supporting Citations
A method for pairwise sequencing of **first and second regions** of a double stranded polynucleotide wherein said **first and second regions** are in the same target double stranded polynucleotide, the method comprising hybridising and reading from a first primer, removing the first primer followed by hybridising and reading from a second primer at a different location in the same target double stranded polynucleotide.	**"first and second regions"** means "two distinct and separate single-stranded portions" **Intrinsic Evidence:**[1] '930 patent figures 1, 8. '930 patent specification at Abstract; 1:19–23; 2:54–59; 3:19–26; 4:21–24; 5:51–58; 8:49–9:2; 9:44–50; 13:20–33; 21:11–18; 21:26–31; 22:30–35. **Extrinsic Evidence:**[2] Deposition of Colin Barnes: 118:13–23; 232:6–21. Deposition of Eric Vermaas: 134:13–136:24; 174:8–175:22; 162:12–163:23; 179:1–25; 202:22–203:18.	**"first and second regions"** means "two distinct portions of the target double-stranded polynucleotide for sequence determination. The first and second regions for sequence determination are either on the same strand, or on complementary strands, of the double-stranded polynucleotide template." **Intrinsic Evidence**: '930 patent: 3:22-31; 3:32-63; 3:64-4:2; 4:3-15; 4:16-24; 5:51-58; 5:59-6:2; 8:49-54; 8:58-9:2; 9:44-50; 13:27-33; 21:11-18; 21:24-31; Examples 5-7; Figures 1, 4, 12. **Extrinsic Evidence**:[3] Deposition of Colin Barnes: 117:9-25. Deposition of Eric Vermaas: 130:5-16; 136:21-24; 162:19-163:2.

[1] The intrinsic evidence identified in this Joint Claim Chart is exemplary. The parties may rely on any portion of the asserted '930 patent and its prosecution history whether or not expressly identified in this Joint Claim Chart.

[2] Illumina does not agree that testimony of the inventors is relevant to claim construction. Illumina cites inventor deposition testimony only to rebut CGI's citations, and Illumina may rely on uncited portions of the inventor deposition testimony to rebut CGI's arguments or provide context and background or to aid in the understanding of the cited portions.

[3] CGI has identified the most relevant portions of the inventor deposition testimony. CGI may rely on uncited portions of the inventor deposition testimony to rebut Illumina's arguments or to provide context and background or to aid in the understanding of the cited portions.

Claim 1	Illumina's Proposed Constructions and Supporting Citations	CGI's Proposed Constructions and Supporting Citations
A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are **in the same target double stranded polynucleotide**, the method comprising hybridising and reading from a first primer, removing the first primer followed by hybridising and reading from a second primer at a different location **in the same target double stranded polynucleotide**.	**"in the same target double stranded polynucleotide"** means "in the same strand or complementary strands derived from the original polynucleotide duplex from which sequencing information is desired" **Intrinsic Evidence:** '930 patent figures 1, 8–12. '930 patent specification at 5:51–6:25; 6:56–7:3; 7:4–25; 8:31–48; 9:26–50; 13:1–33; 14:65–15:3; 19:6–11; 22:18–31; 26:52–54; 29:43–30:34 (Example 4). '930 patent claims 1–26. '930 patent file history, August 7, 2008 Preliminary Amendment; March 4, 2011 Office Action, pages 5–10; June 6, 2011 Amendment and Response, pages 6–9; September 7, 2011 Office Action, pages 5–10, 18–22. **Extrinsic Evidence:** Deposition of Colin Barnes: 154:17–159:20; 185:5–188:22; 191:2–192:23. Deposition of Jonathan Boutell: 175:5–18. Deposition of Eric Vermaas: 165:3–169:9; 169:15–173:15; 174:8–175:12; 179:1–180:11; 249:1–17.	**"in the same target double stranded polynucleotide"** means "in the template polynucleotide duplex formed from complementary first and second template strands which are linked to the solid support at or near their 5' ends" **Intrinsic Evidence**: '930 patent: 3:4-63; 3:64-4:2; 4:3-15; 4:16-24; 5:51-6:2; 8:58-9:2; 9:42-50; 10:54-60; 13:1-33; 20:49-21:3; 22:37-58; Examples 3-7; Figures 1, 8, 12. '930 patent file history: August 7, 2008 Preliminary Amendment, page 8. **Extrinsic Evidence**: Deposition of Colin Barnes: 81:9-82:5; 158:2-159:20; 185:5-13; 189:22-190:25; 202:13-205:20. Deposition of Jonathan Boutell: 173:22-175:4; 177:17-23; 179:2-19; 187:14-188:8; 194:2-6. Deposition of Eric Vermaas: 168:7-169:9; 171:25-172:6; 175:6-12; 180:6-11; 202:22-203:22.

Claim 1	Illumina's Proposed Constructions and Supporting Citations	CGI's Proposed Constructions and Supporting Citations
A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising hybridising and **reading from a first primer**, removing the first primer followed by hybridising and **reading from a second primer** at a different location in the same target double stranded polynucleotide.	**"reading from a [first/second] primer"** means "obtaining sequence information near where the [first/second] primer has hybridized" **Intrinsic Evidence:** '930 patent figures 1, 8. '930 patent specification at 2:1–21; 3:20–31; 6:41–48; 8:49–9:7; 21:32–22:17 (including U.S. Pat. No. 6,306,597); 30:35–32:67. '930 patent claims 1–26. U.S. Pub. No. 2003/0022207 A1, Balasubramanian et al., 1/30/2003. **Extrinsic Evidence:** [4] Deposition of Colin Barnes: 185:5–188:22; 191:2–192:23. Deposition of Eric Vermaas: 154:2–157:18; 179:1–180:25. Michael L. Metzker, *Sequencing Technologies—the Next Generation*, Nature Reviews Genetics 31-46 (January 2010). *See, e.g.*, Figure 3 and accompanying text. *The Race for the $1000 Genome*, 311 Science 1544 (Mar. 17, 2006). *See, e.g.*, page 1545.	**"reading from a [first/second] primer"** means "the successive incorporation of nucleotides into a polynucleotide chain synthesized in the 5' to 3' direction from the [first/second] primer and the determination of the nature of the nucleotide after each incorporation" **Intrinsic Evidence**: '930 patent: 3:32-63; 21:13-18; 21:24-31; 21:32-38; 21:43-51; 22:9-13; Examples 5-7; Figure 1. '930 patent file history: August 7, 2008 Preliminary Amendment, page 8. **Extrinsic Evidence**: "Primer DNA: 1. single-stranded DNA required for replication by DNA polymerase III. . . 2. Oligonucleotides of single-stranded DNA synthesized by a gene machine for use in a polymerase chain reaction." A Dictionary of Genetics (2006), page 354. Deposition of Colin Barnes: 185:5-13. Deposition of Eric Vermaas: 157:7-18; 180:19-25. U.S. Patent No. 6,306,597 Mostafa Ronaghi, *Pyrosequencing Sheds Light on DNA Sequencing*, Genome Research 11:3-11 (2001).

[4] Illumina objects to CGI's citation to the Ronaghi, Brenner, and Mitra articles as extrinsic evidence because CGI failed to either identify or produce copies of any of these extrinsic references until 5:48 P.M. on April 16, 2013, the day this Joint Claim Construction Chart was due.

	Jay Shendure, et al., *Accurate Multiplex Polony* Sequencing *of an Evolved Bacterial Genome*, 309 Science 1728-1732 (2005). *See, e.g.*, page 1729. WIPO patent application WO 2006/073504. *See, e.g.*, Example V. Martin Kircher & Janet Kelso, *High-Throughput DNA Sequencing-Concepts and Limitations*, 32 Bioessays 524-536 (2010). *See, e.g.*, Figure 4 and accompanying text.	Sydney Brenner, at al., *Gene expression analysis by massively parallel signature sequencing (MPSS) on microbead arrays*, Nature 18:630-634 (2000). Robi D. Mitra, et al., *Fluorescent in situ sequencing on polymerase colonies*, Analytical Biochemistry 320:55-65 (2003).

Claim 1	Illumina's Proposed Constructions and Supporting Citations	CGI's Proposed Constructions and Supporting Citations
A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising hybridising and reading from a first primer, **removing the first primer** followed by hybridising and reading from a second primer at a different location in the same target double stranded polynucleotide.	**"removing the first primer"** need not be construed, or if construed, the Court should construe this phrase as having its plain and ordinary meaning. **Intrinsic Evidence:** '930 patent figures 1, 8. '930 patent specification at 9:3–7; 13:27–33.	**"removing the first primer"** means "heating or chemically denaturing from the surface the first sequencing primer when the first sequencing reaction is complete." **Intrinsic Evidence**: '930 patent: 3:32-63; 3:66-4:2; 9:3-7; 13:12-15; 13:27-33; 21:24-31; Examples 5-7; Figure 1.

Claim 1	Illumina's Proposed Constructions and Supporting Citations	CGI's Proposed Constructions and Supporting Citations
A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising hybridising and reading from a first primer, removing the first primer followed by hybridising and reading from a second primer at a **different location** in the same target double stranded polynucleotide.	**"different location"** means "a location distinct and separate from the location of hybridizing and reading from the first primer" **Intrinsic Evidence:** '930 patent figures 1, 8. '930 patent specification at Abstract; 1:19–23; 2:5–30; 3:19–31; 4:3–24; 5:54–58; 8:31–36; 8:49–9:7; 13:20–33; 30:35–32:67. **Extrinsic Evidence:** Deposition of Eric Vermaas: 162:19–163:10.	**"different location"** means "location of the second region that is distinct from the first region" **Intrinsic Evidence**: '930 patent: 3:22-31; 3:32-63; 3:64-4:2; 4:3-15; 4:16-24; 8:49-54; 8:58-9:2; 9:44-50; 13:27-33; Examples 5-7; Figures 1, 12. **Extrinsic Evidence:** Deposition of Eric Vermaas: 130:5-16; 162:19-163:2.

SIGNATURE CERTIFICATION

Pursuant to Section 2(f)(4) of the Electronic Case Filing Administrative Policies and Procedures Manual, I hereby certify that the content of this document is acceptable to Michael J. Malecek, counsel for Defendant and Counterclaimant Complete Genomics, Inc., and that I have obtained Mr. Malecek's authorization to affix his electronic signature to this document.

Dated: April 16, 2013

Respectfully submitted,
MARSHALL, GERSTEIN & BORUN LLP

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